Agri-Tech Innovation Ecosystem Workshop

Outline

I. **Introduction and remarks.** Professor Owen Atkin, Division Head, Plant Sciences, ANU (5 minutes)

II. **The changing agri-tech landscape.** Rob Elshire, President Genomics For Aotearoa New Zealand (25 minutes)

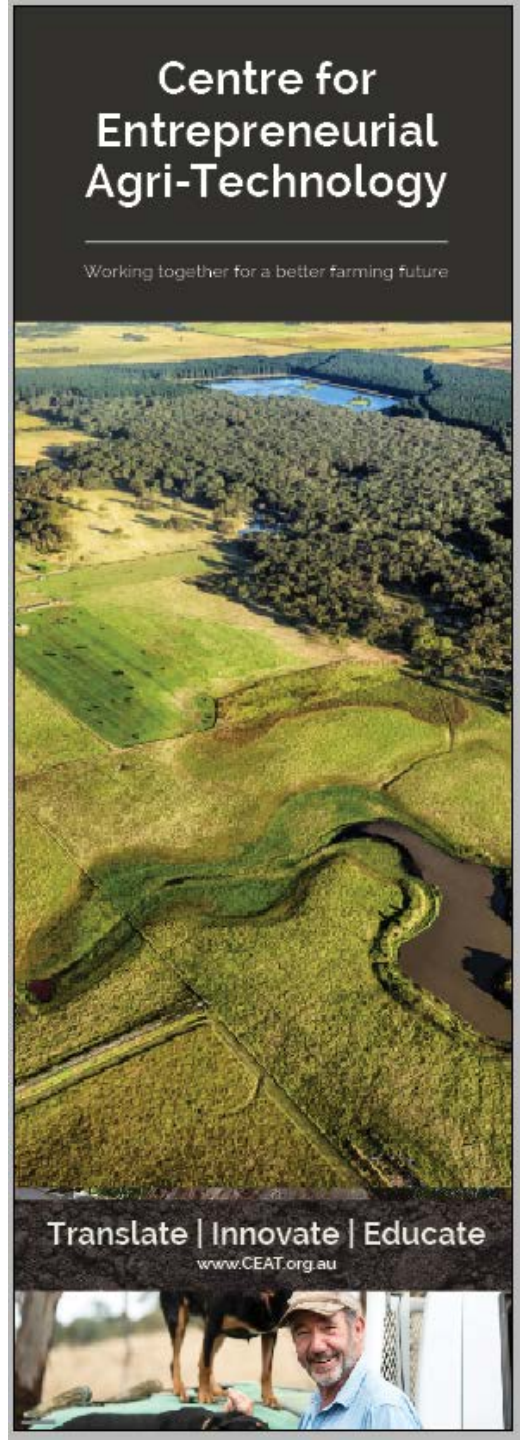
III. **Emerging opportunities.** Rob Elshire, President Genomics For Aotearoa New Zealand (30 minutes)

IV. **New Zealand agri-ecological example.** Professor Justin Borevitz, Plant Genomics for Climate Adaptation, ANU, and Rob Elshire, President Genomics For Aotearoa New Zealand (45 minutes)

V. **Better ways of working together.** Rob Elshire, President Genomics For Aotearoa New Zealand (45 minutes)

I. **Discussion.** Facilitated by Professor Owen Atkin, Division Head, Plant Sciences, ANU (30 minutes)

Venue: Jan Anderson Seminar room, Robertson Building, #46, ANU, 46 Sullivans Creek Road, Acton, Canberra (campus map here)
Date: Tuesday, 4 September, 2018
Time: 2pm-4:30pm
Contact: Dr Emma Burns, Senior Project Manager, CEAT. Phone: 0415657485 Email: emma.burns@anu.edu.au



Convenor Bios

Rob Elshire, President Genomics For Aotearoa New Zealand

Rob began his work in agriculture with the simple idea that he could use his skills and interests to help address the basic human need for food. The interdisciplinary field of plant breeding offered an opportunity to combine working with plants, maths, and computers. Along the way, he had the great fortune of joining a group of like minded people in the Buckler lab at Cornell. There, in 2007 and 2008, he cut his teeth on the nascent Illumina GA sequencing platform and designed a set of library preps to avoid most of the repetitive fraction of the maize genome. The resulting maize hap map paper was published in *Science* in 2009.

Building on that work, he developed a simple, low cost, highly multiplexed genotyping-by-sequencing (GBS) method which he and his colleagues made every effort to make easy to use and share with anyone who was interested. When he had demonstrated to his group that they had a robust and scalable protocol, they sent it to about 20 other labs, including the Borevitz lab, for review in their hands. They then published it in PLoS ONE so that anyone with a web browser could access their work. He designed and conducted the early workshops on GBS which were held free of charge. Later, he wrote the planning document for and helped implement the GBS service at Cornell so that groups with small projects could easily use the technology. In his last years at Cornell, he coordinated the team that developed software to analyse GBS data, managed a maize genotyping project across 5 continents, wrote scripts to run the analyses in an auditable way, and personally conducted the bioinformatic analysis of over 30,000 maize samples.

The GBS method has proven to be robust and widely applicable. During the time it operated, the GBS service at Cornell generated data on over 300 species. It has been used in breeding programmes (both public and private) for all of the major plant commodity crops and many agricultural animal species as well. Beyond agriculture, GBS has been broadly used in ecological and conservation biology studies. The paper has over 1700 citations as reported by SCOPUS. The simplicity of the method coupled with the way they released it has democratised the production of genomic data across the board.

Rob is very happy to have contributed in this way to the advancement of genomics technologies. At the same time, there is much more work to be done. In the computational space, there are still many hurdles to effective and affordable use of the tools. In his view, the time is ripe for the adoption of cloud computing and cloud native tools to democratise the analysis. Rob and colleagues are building that infrastructure in New Zealand's public cloud now.

By making the whole set of tools open-source, they can enable the development of an ecosystem of small nimble companies in the Agri-Tech space. The barriers to entry can be reduced to the extent that smart, talented individuals can create new companies today without the huge investment in equipment and infrastructure that was required just 5 years ago. This is starting to happen now and Rob is keen to share how it can be done with others.

Convenor Bios

Professor Justin Borevitz
Plant Genomics for Climate Adaptation
ANU

Australian National University

Professor Borevitz obtained his PhD in 2002 from the University of California at San Diego with Joanne Chory studying Natural Variation in Arabidopsis light response. His postdoctoral research was with Joseph Ecker (2002-2004) at the Salk Institute focused on genomic diversity in Arabidopsis using tiling microarrays. He then started as assistant and associate professor in the Department of Ecology and Evolution at the University of Chicago (2004 until 2012). His research focused on Genome Wide Association Studies in Arabidopsis and next generation genotyping by sequencing in emerging model organisms. In 2012, he started at the ANU where his current work is identifying the genetic basis of local adaptation to seasonal climates using Phenomic and Landscape Genomic approaches in plant model organisms and foundation species.

Web: https://borevitzlab.anu.edu.au

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Abstract

It is an incredible time in the field of Agricultural Technology. We have a data rich environment that has been created through low cost and ubiquitous technology such as DNA sequencers, cloud computing, mobile phones, and internet-of-things sensing devices. Opportunities abound for using all this data to improve agricultural outcomes. At the same time, government research funding is tight all across the globe, making it more and more difficult for our well trained young people to find work in their fields at home.

This workshop will take a broad look at the changing landscape of Agri-Tech, offers insights into how innovation can be fostered, and provides an example of how an Agri-Tech ecosystem can add enormous value to the small business community. It will also suggest ways that individuals and institutions can engage with one another to create this kind of ecosystem.